

Yu Hu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9174845/publications.pdf>

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13
papers

527
citations

1040056

9
h-index

1199594

12
g-index

16
all docs

16
docs citations

16
times ranked

1039
citing authors

#	ARTICLE	IF	CITATIONS
1	LIQA: long-read isoform quantification and analysis. <i>Genome Biology</i> , 2021, 22, 182.	8.8	49
2	Implications of Error-Prone Long-Read Whole-Genome Shotgun Sequencing on Characterizing Reference Microbiomes. <i>IScience</i> , 2020, 23, 101223.	4.1	10
3	Detecting differential alternative splicing events in scRNA-seq with or without Unique Molecular Identifiers. <i>PLoS Computational Biology</i> , 2020, 16, e1007925.	3.2	20
4	LongGF: computational algorithm and software tool for fast and accurate detection of gene fusions by long-read transcriptome sequencing. <i>BMC Genomics</i> , 2020, 21, 793.	2.8	22
5	PennDiff: detecting differential alternative splicing and transcription by RNA sequencing. <i>Bioinformatics</i> , 2018, 34, 2384-2391.	4.1	14
6	Accounting for technical noise in differential expression analysis of single-cell RNA sequencing data. <i>Nucleic Acids Research</i> , 2017, 45, 10978-10988.	14.5	73
7	Adipose tissue RNASeq reveals novel gene-nutrient interactions following n-3 PUFA supplementation and evoked inflammation in humans. <i>Journal of Nutritional Biochemistry</i> , 2016, 30, 126-132.	4.2	30
8	Transcriptome-Wide Analysis Reveals Modulation of Human Macrophage Inflammatory Phenotype Through Alternative Splicing. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2016, 36, 1434-1447.	2.4	35
9	Mapping Splicing Quantitative Trait Loci in RNA-Seq. <i>Cancer Informatics</i> , 2015, 14s1, CIN.S24832.	1.9	7
10	RNA-Seq identifies novel myocardial gene expression signatures of heart failure. <i>Genomics</i> , 2015, 105, 83-89.	2.9	220
11	Mapping Splicing Quantitative Trait Loci in RNA-Seq. <i>Cancer Informatics</i> , 2014, 13s4, CIN.S13971.	1.9	6
12	Exploring strategy selection in populations via a continuous evolutionary game dynamics. , 2014, , .		3
13	PennSeq: accurate isoform-specific gene expression quantification in RNA-Seq by modeling non-uniform read distribution. <i>Nucleic Acids Research</i> , 2014, 42, e20-e20.	14.5	33